

FIGURE 1A

9.1 (SEQ ID NO:1): 5' GGGAGAGAGG AAGAGGGAUG GG CCGCCAGU  
GGGAAGCUAU ACCCAACGCC CCAGCCCCAG AGCAUAACCC AGAGGUUCGAU AGUACUGGAU  
CCCCCC 3'

9.2 (SEQ ID NO:2): 5' GGGAGAGAGG AAGAGGGAUG GGCUAUAUAC ACGCUGGUGA  
UCCCAUCUCA AUUGAAACAA CACAUAAACCC AGAGGUUCGAU AGUACUGGAU CCCCCC 3'

9.3 (SEQ ID NO:3): 5' GGGAGAGAGG AAGAGGGAUG GGGACUAUAC CGCGUAAUGC  
UGCCUCCCCA UUCCGGAACG CUCAUAACCC AGAGGUUCGAU AGUACUGGAU CCCCCC 3'

9.4 (SEQ ID NO:4): 5' GGGAGAGAGG AAGAGGGAUG GGCACUAUAC GCAUCUJGCU  
GCCUGCCCCG GAGUAAAUU GCAUAACCC GAGGUUCGAU GUACUGGAU CCCCCC 3'

9.5 (SEQ ID NO:5): 5' GGGAGAGAGG AAGAGGGAUG GGCCUACCAAG UUCGUGGCUA  
GCGUGACGUA CCACCCAGGG ACCAUAAACCC AGAGGUUCGAU AGUACUGGAU CCCCCC 3'

9.7 (SEQ ID NO:6): 5' GGGAGAGAGG AAGAGGGAUG GGCGAUAACC AACAUUGGUGA  
UCCCAUUCAU CAUACCUAC AACAUAAACCC AGAGGUUCGAU AGUACUGGAU CCCCCC 3'

9.8 (SEQ ID NO:7): 5' GGGAGAGAGG AAGAGGGAUG GGGCCACCUA CUAUACCGGU  
CAUCGUGCAU AGGUCGCUGC CACAUAAACCC AGAGGUUCGAU AGUACUGGAU CCCCCC 3'

9.9 (SEQ ID NO:8): 5' GGGAGAGAGG AAGAGGGAUG GGUCUCACAC CCGAAGAUGG  
CCAAAGAGGG AGAUGAGUUU CCAUAACCC GAGGUUCGAU GUACUGGAU CCCCCC 3'

9.11 (SEQ ID NO:9): 5' GGGAGAGAGG AAGAGGGAUG GGACUAUAUJ CGGAAUCUGG  
ACUCCCACCU GCCUGCCCCA GACAUAAACCC AGAGGUUCGAU AGUACUGGAU CCCCCC 3'

9.12 (SEQ ID NO:10): 5' GGGAGAGAGG AAGAGGGAUG GGCGAUUAUAC  
ACAUUGGUGA UCCCACCCAC AUGAAACCAAC AGCAUAACCC AGAGGUUCGAU AGUACUGGAU  
CCCCCC 3'

9.13 (SEQ ID NO:11): 5' GGGAGAGAGG AAGAGGGAUG GGCUCAUCAC  
AGGCAGAAGUG AACAAACACUA CCGNCNAGUU ACCAUAAACCC AGAGGUUCGAU AGUACUGGAU  
CCCCCC 3'

9.14 (SEQ ID NO:12): 5' GGGAGAGAGG AAGAGGGAUG GG GACUAUAC  
GUGAACGACU GCAUCCACUUC CCCGCCAUGG CAUAACCCAG AGGUCGAUAG  
UACUGGAUCC CCCC 3'

FIGURE 1B

9.16 (SEQ ID NO:13): 5' GGGAGAGAGG AAGAGGGAUG GGCAUACGU  
GGACGACUGC ACCCGACCCU UCAGCCCAGG UCCAUAAACCC AGAGGUCGAU AGUACUGGAU  
CCCCCC 3'

9.17 (SEQ ID NO:14): 5' GGGAGAGAGG AAGAGGGAUG GGACCAUACG  
CACAUUGCUG AAUCCCCUC AAUAGCACCU ACCAUAAACCC AGAGGUCGAU AGUACUGGAU  
CCCCCC 3'

9.18 (SEQ ID NO:15): 5' GGGAGAGAGG AAGAGGGAUG GGCAUAACC  
ACUUUGGUGA ACCCACCCAG CUCC/UUGUGAU UGCAUAAACCC AGAGGUCGAU  
AGUACUGGAU CCCCCC 3'

9.19 (SEQ ID NO:16): 5' GGGAGAGAGG AAGAGGGAUG GGACCAUAAC  
GACUACUCGUGA AUCCCCCAU CAGCGCACAA CAUAACCCAGA GGUCGAUAG  
UACUGGAUCC CCCC 3'

9.20 (SEQ ID NO:17): 5' GGGAGAGAGG AAGAGGGAUG GGGACUAUAC  
CGGCÀAUCGU GCAUCCCCUG GACCUAACAA UACAUAAACCC AGAGGUCGAU AGUACUGGAU  
CCCCCC 3'

9.21 (SEQ ID NO:18): 5' GGGAGAGAGG AAGAGGGAUG GG AACACCAU  
UAAAUGCUCGG CCAGGUAAACC CCGGCGCAUA CUCAUAAACCC AGAGGUCGAU AGUACUGGAU  
CCCCCC 3'

9.25 (SEQ ID NO:19): 5' GGGAGAGAGG AAGAGGGAUG GGGACCAUAA  
CUCUAACGGG UGAAUCCCGC AUCUCGACAA UACAUAAACCC AGAGGUCGAU AGUACUGGAU  
CCCCCC 3'

9.26 (SEQ ID NO:20): 5' GGGAGAGAGG AAGAGGGAUG GG UGAUAACC  
ACUCUGGUGA ACCCCUCCCG ACUUGCUCGC ACAUAACCCCA GAGGUCGAUA GUACUGGAUC  
CCCCCC 3'

9.27 (SEQ ID NO:21): 5' GGGAGAGAGG AAGAGGGAUG GGUAUAACU  
GUAUGGUGAA CCCACCCAAA CUCCAUGGC UACAUAAACCC AGAGGUCGAU AGUACUGGAU  
CCCCCC 3'

9.28 (SEQ ID NO:22): 5' GGGAGAGAGG AAGAGGGAUG GG CGCCAUAC  
GCACAUJGGCU GCAUCGCCUU CCCGUAAGAA CCAUAACCCCA GAGGUCGAUA GUACUGGAUC  
CCCCCC 3'

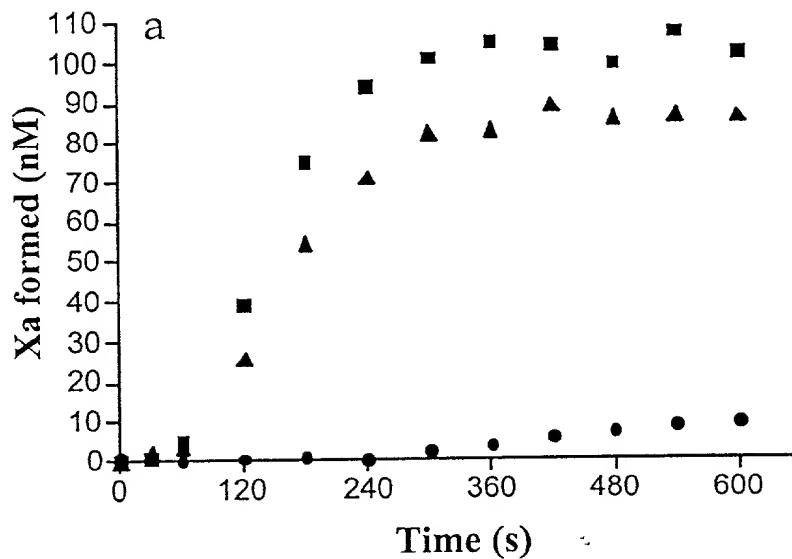
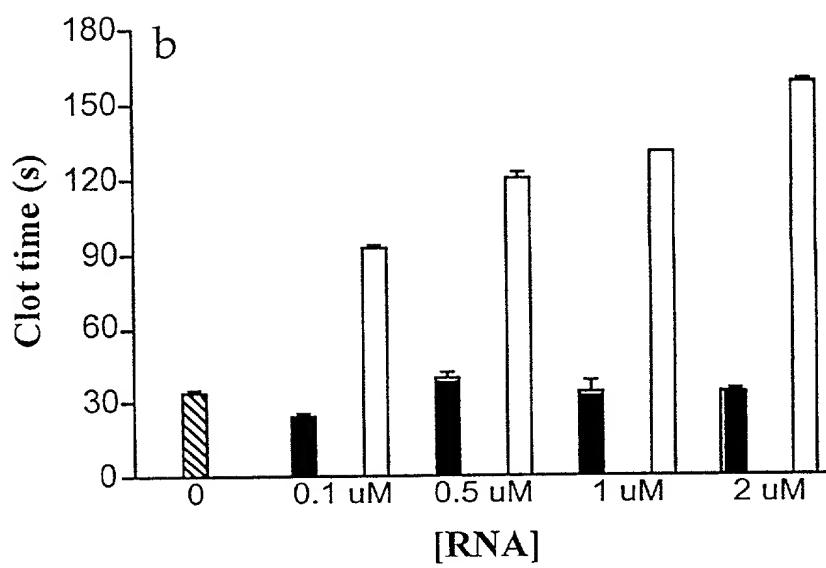


FIGURE 2A

FIGURE 2B



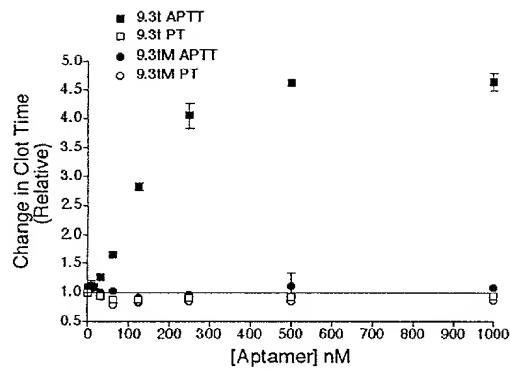


Figure 3A

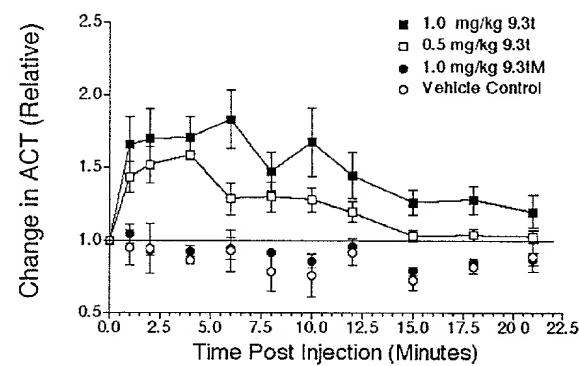


Figure 3B

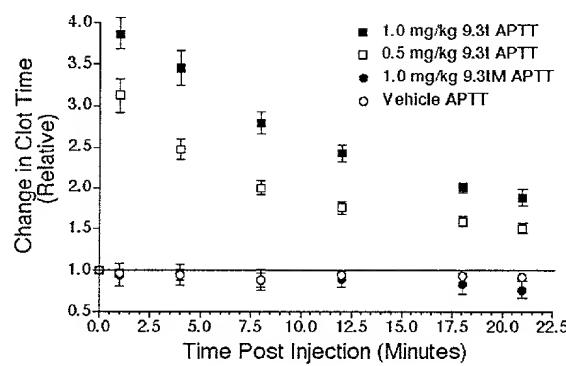


Figure 3C

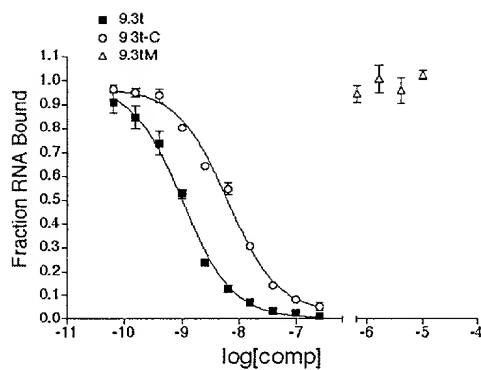


Figure 4A

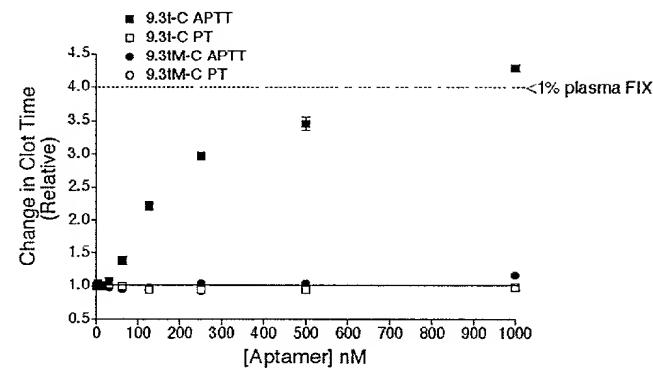


Figure 4B

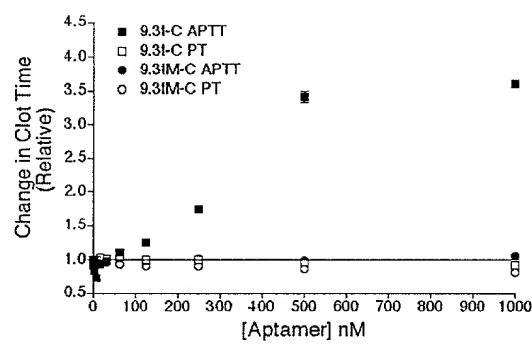


Figure 4C

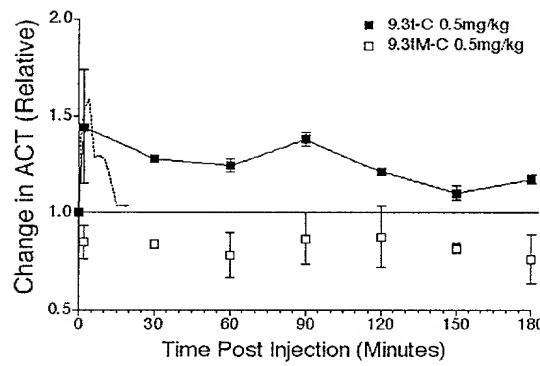


Figure 5A

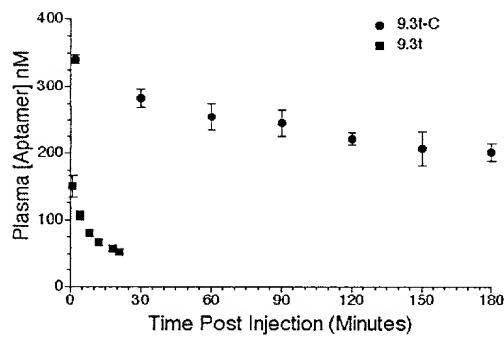


Figure 5B

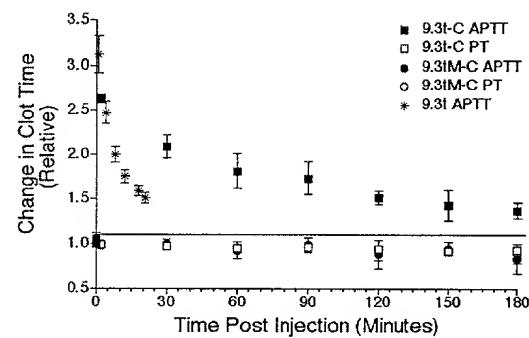


Figure 5C

Figure 6A

10.1 (SEQ ID NO:23): 5' GGGAGAGAGG AAGAGGGAUG GGAAAAUAGC  
CCCAGCGAGA UAAUACUUGG CCCCCGUACCA CCAUAACCCA GAGGUCGAUA  
GUACUGGAUC CCCCC 3'

10.5 (SEQ ID NO:24): 5' GGGAGAGAGG AAGAGGGAUG GGCCAGAAGG  
AACUAAACAC CUGAACCCCC CAUCGCGAGAG ACCAUAAACCC AGAGGUCGAU  
AGUACUGGAU CCCCCC 3'

10.6 (SEQ ID NO:25): 5' GGGAGAGAGG AAGAGGGAUG GGAUGUCACU  
UGGCCCUUCG CGCACc/aCGCC AGCGAGCCCA UAACCCAGAG GUCGAUAGUA  
CUGGAUCCCC CC 3'

10.7 (SEQ ID NO:26): 5' GGGAGAGAGG AAGAGGGAUG GGACACGCC  
AGCGAGCUA AACUUGGCC CCGUGCAUCA CC CCAUAACC CAGAGGUCGA  
UAGUACUGGA UCCCCC 3'

10.8 (SEQ ID NO:27): 5' GGGAGAGAGG AAGAGGGAUG GGAAGUGCCA  
CAGCGAGCAC AUGACUUGGC CCCGCAUUGC ACCAUAAACC CAGAGGUCGA UAGUACUGGA  
UCCCCC 3'

10.11 (SEQ ID NO:28): 5' GGGAGAGAGG AAGAGGGAUG GGAAACUAAU  
GCCCUAGCGA GCAUACCCGG ACUGGCCCG CCAUAACCC AGAGGUCGAU AGUACUGGAU  
CCCCCC 3'

10.12 (SEQ ID NO:29): 5' GGGAGAGAGG AAGAGGGAUG GGAAAAUAGC  
CCCAGCGAGA UAAUACUUGG CCCCCGUACU ACCAUAAACC CAGAGGUCGA UAGUACUGGA  
UCCCCC 3'

10.13 (SEQ ID NO:30): 5' GGGAGAGAGG AAGAGGGAUG GGCGACCCCA  
CUGGCGGAAA CCGACAAUCA CUCCCCACGA CCAUAACCC AGAGGUCGAU AGUACUGGAU  
CCCCCC 3'

10.14 (SEQ ID NO:73): 5' GGGAGAGAGG AAGAGGGAUG GGAAAAUAGC  
CCCAGCGAGA UAAUACUUGG CCCCCGUACU ACCAUAAACCC AGAGGUCGAU AGUACUGGAU  
CC 3'

Figure 6B

10.15 (SEQ ID NO:31) : 5' GGGAGAGAGG AAGAGGGAUG GGCAAGCCCAG  
CGAGGGACAC UUAACCCCCU GUCCCCAUC CAAACAUAA CCCAGAGGUC GAUAGUACUG  
GAUCCCCCC 3'

10.18 (SEQ ID NO:32) : 5' GGGAGAGAGG AAGAGGGAUG GGCCAGAACGU  
CACCGCGACG GUACUGAACCC ACCCAUAACC CAGAGGUCGA UAGUACUGGA  
UCCCCCCC 3'

10.19 (SEQ ID NO:33) : 5' GGGAGAGAGG AAGAGGGAUG GGCCAGAACGU  
GCUCACUACA ACGCUUUGAC CCCCCCAUCC ACAUCCAUAA ACCCAGAGGU CGAUAGUACU  
GGAUCCCCCC 3'

10.21 (SEQ ID NO:34) : 5' GGGAGAGAGG AAGAGGGAUG GG CCAGCAAC  
CGAAGGGCGG AAUACCCCCC GUCUCCACAU ACCCAUAACC CAGAGGUCGA UAGUACUGGA  
UCCCCCCC 3'

10.22 (SEQ ID NO:35) : 5' GGGAGAGAGG AAGAGGGAUG GG ACGCGACU  
CAGGCAGCAC UUGACUUGGC CCCUUGCGAU CACCAUAACC CAGAGGUCGA UAGUACUGGA  
UCCCCCCC 3'

10.23 (SEQ ID NO:36) : 5' GGGAGAGAGG AAGAGGGAUG GG CCAGCAAC  
GCUAACACGG AAUACCCCCC ACCCAACGU GCCCAUAACC CAGAGGUCGA UAGUACUGGA  
UCCCCCCC 3'

10.24 (SEQ ID NO:37) : 5' GGGAGAGAGG AAGAGGGAUG GG CUUCUCAA  
CCGAAAUACA ACUUUAAAUC AUUUUAUCACU UACCAUAACC CAGAGGUCGA UAGUACUGGA  
UCCCCCCC 3'

10.30 (SEQ ID NO:38) : 5' GGGAGAGAGG AAGAGGGAUG GGAAUACGCCG  
AUGCAAGCAU GUCCACACAC CGCAUGCCGU ACCCAUAACC CAGAGGUCGA UAGUACUGGA  
UCCCCCCC 3'

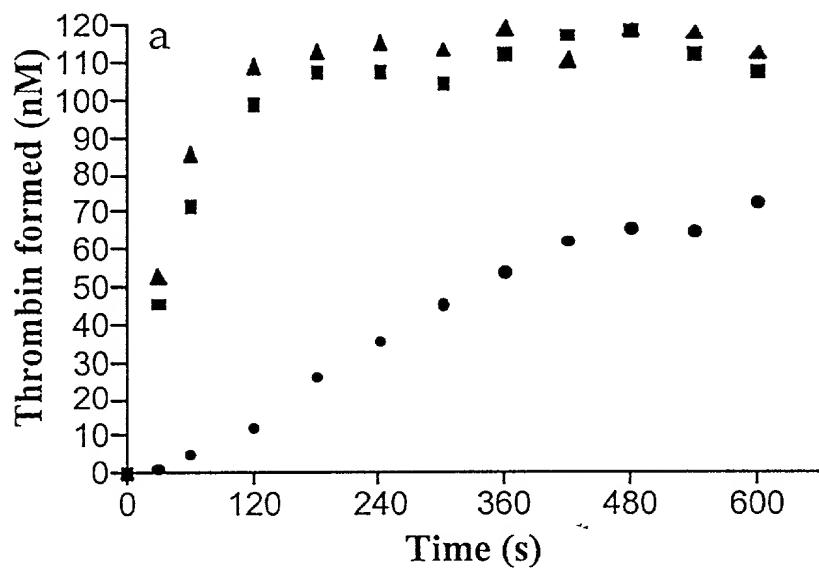
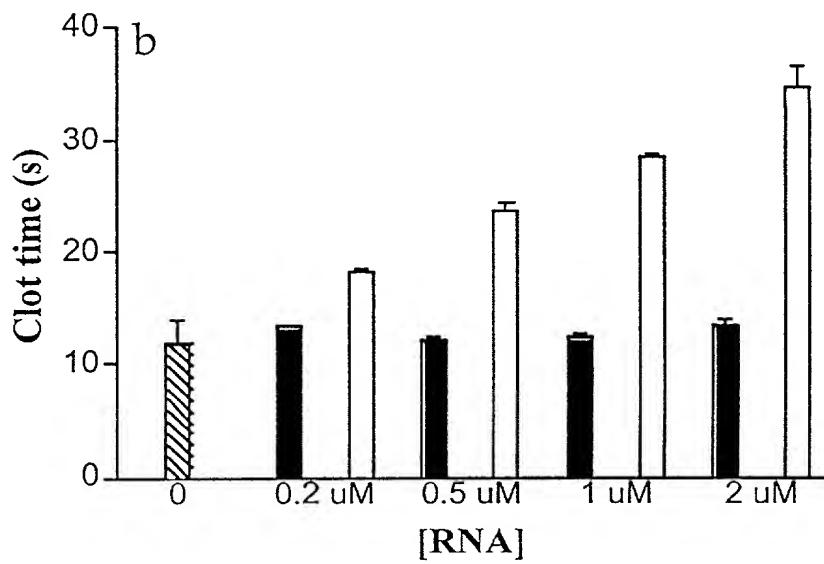


Figure 7A

Figure 7B



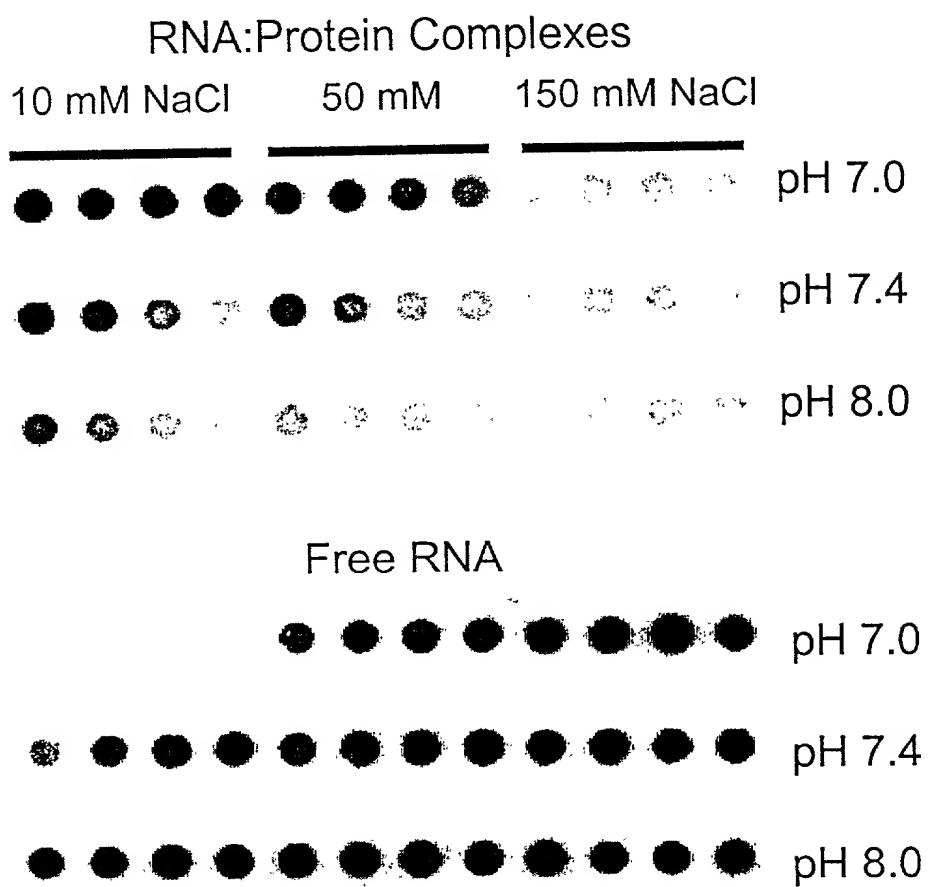
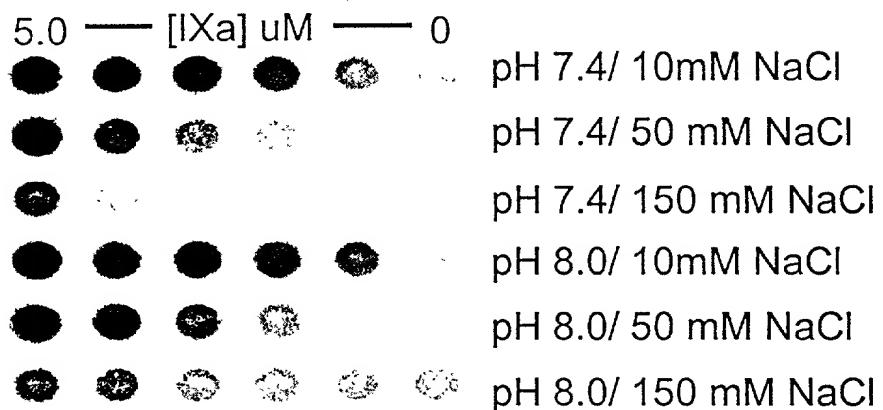


FIGURE 8

### RNA:Protein Complexes



### Free RNA

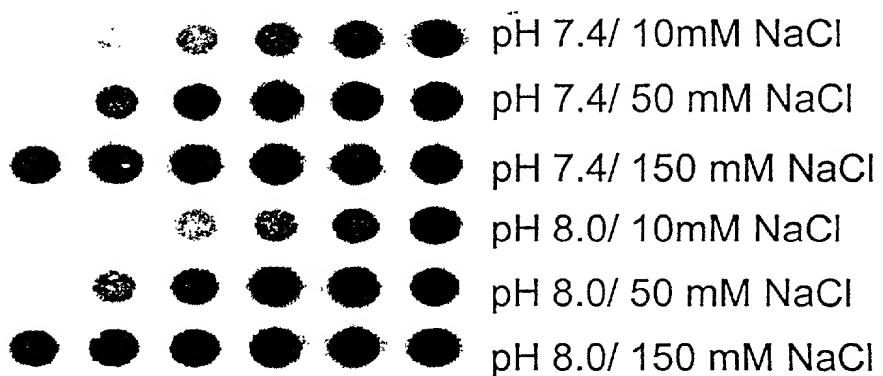


FIGURE 9

Figure 10

16.1: (SEQ ID NO:39) 5' GGGAGAGAGG AAGAGGGAUG GGUACAGAGG AGUACAAGUA  
GCAUGGUCCC CUCGUGUAAA AACAUAAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.2 (SEQ ID NO:40): 5' GGGAGAGAGG AAGAGGGAUG GGUGCAGAAG AGCUUCUUGU  
AGUAUGAUCC CUCAACCGCA AGCAUAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.3 (SEQ ID NO:41): 5' GGGAGAGAGG AAGAGGGAUG GG UACAGAGG AGUACAAGUA  
GCAUGAUCCC CUCGUGUAAA AACAUAAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.5 (SEQ ID NO:42): 5' GGGAGAGAGG AAGAGGGAUG GGAGCCUAUG UAACAGAUGC  
AGAUCCCUAG UCGUCCCAAC ACCAUAAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.7 (SEQ ID NO:43): 5' GGGAGAGAGG AAGAGGGAUG GGCACAACGA ACACCGCAUC  
CCUUGACAGA AAGAGCACGC CUCAUAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.10 (SEQ ID NO:44): 5' GGGAGAGAGG AAGAGGGAUG GGUACAGAGG AGUACAAGUA  
ACAUGAUCCC CUCGUGUAAA AACAUAAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.11 (SEQ ID NO:45): 5' GGGAGAGAGG AAGAGGGAUG GG CACAACGA ACACCGCAUC  
CCUUGACAGA AAGAACACGC CUCAUAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

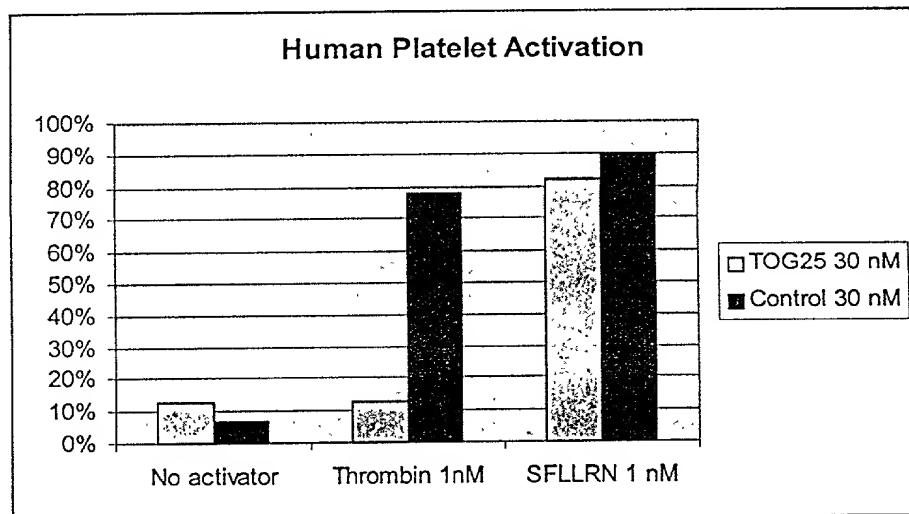
16.18 (SEQ ID NO:46): 5' GGGAGAGAGG AAGAGGGAUG GGCACAAGGA ACACCGCAUC  
CCUUGACAGA AAGAACACGC CUCAUAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.20 (SEQ ID NO:47): 5' GGGAGAGAGG AAGAGGGAUG GGAGCCUAUG UAACAGAUGC  
AGAUCCCUAG ACGACCCAAC ACCAUAAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

FIGURE 11

Random region sequences (Round 13)	K <sub>d</sub> Human Thrombin	K <sub>d</sub> Porcine Thrombin
PIG 5 UGCGAACAAAGCUGAAGUACUUACGCACAACCCGUAGAAU	3 nM	1 nM
PIG 7 AAACACUGAAGAACUACCUUCUUACUGACGAAUUA	1 nM	<0.5 nM
PIG 8 AAACAAAGCUGAACGUACUUAUUCCAUCAUCACCACGCCGGAA	1 nM	0.5 nM
PIG 10 UAUUUGGCUUCUCAGUGCCGCAGAGACAGCAACAAUAGU	>>50 nM	0.5 nM
HUMAN ACAAAGCUGGAGAACUUACCGUUCCCCUCUCCAGAGAUCAA	2 nM	0.5 nM
TOGGLE 25 GAACAAAGCUGAACGUACUUAACCAAGAUCAUCCCACGAA	5 nM	0.5 nM
TOGGLE 30 ACAAAGCUGGAGAACUUAACGUUCCCCUCUCCAGCGGUAA	3 nM	0.5 nM

FIGURE 12



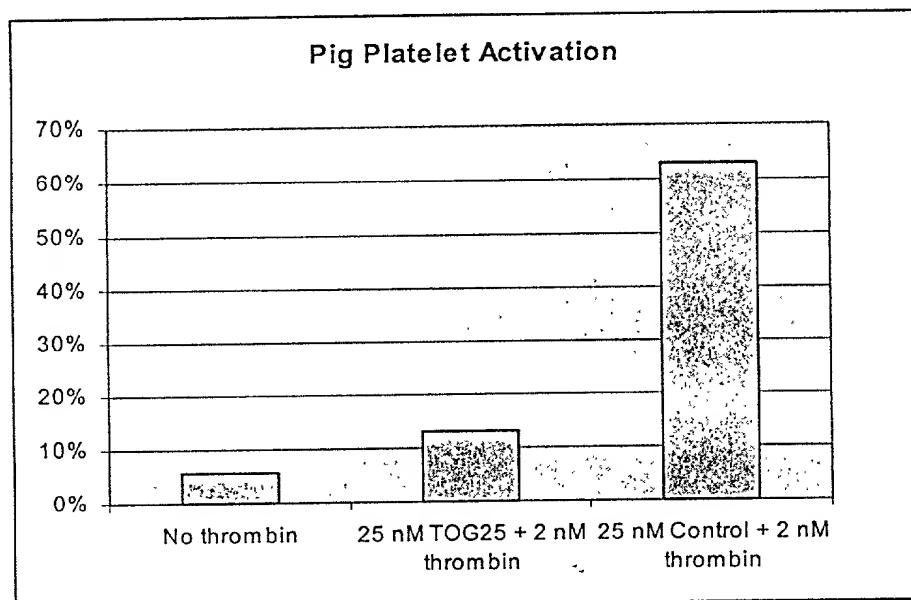


FIGURE 13

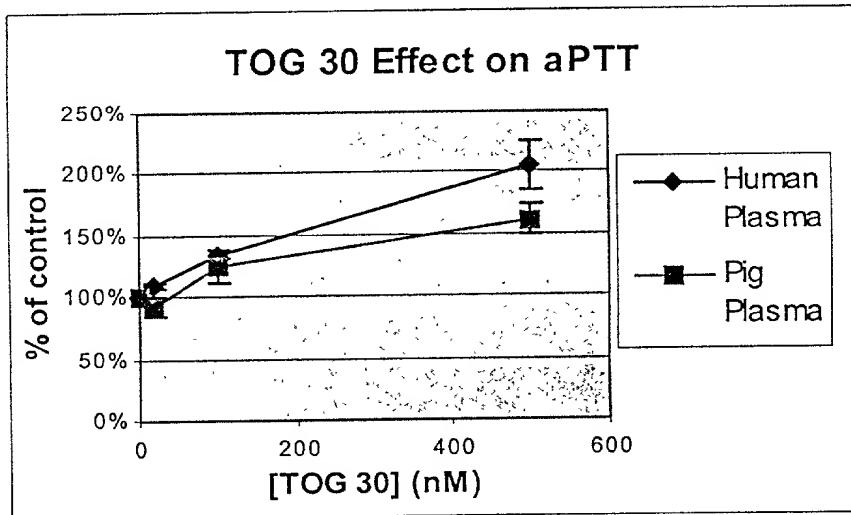


FIGURE 14

Figure 15

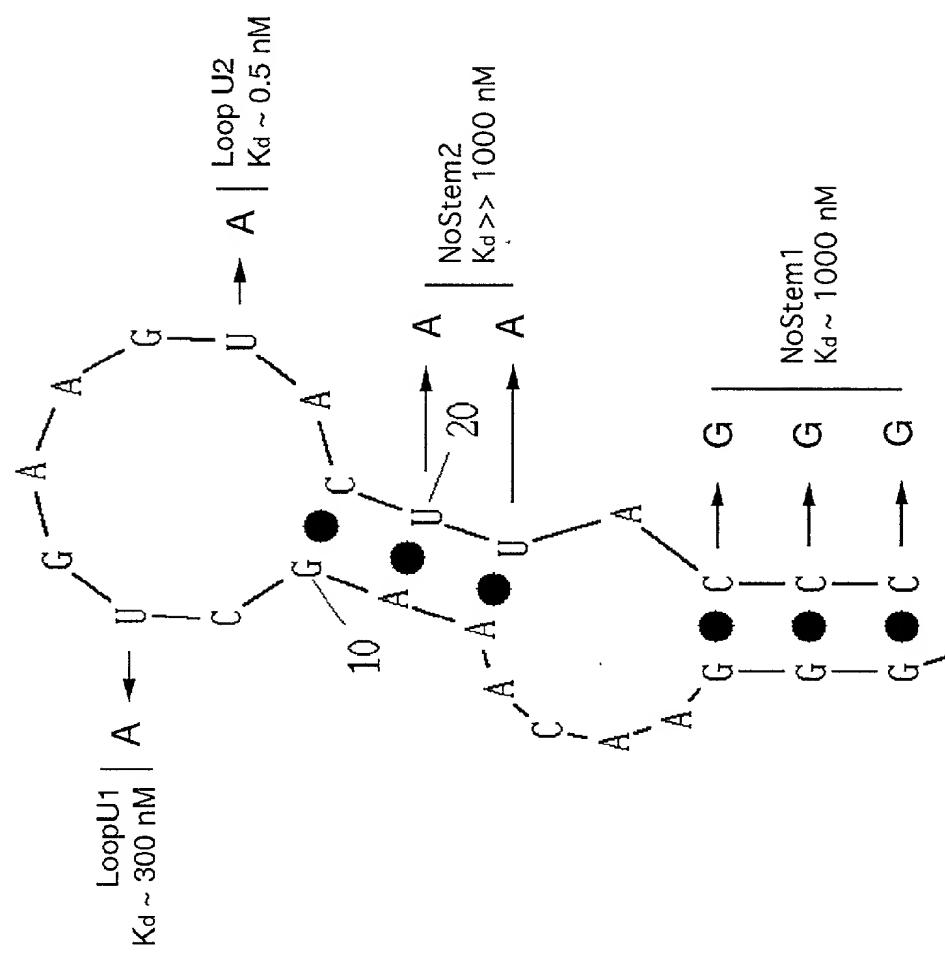


Figure 16

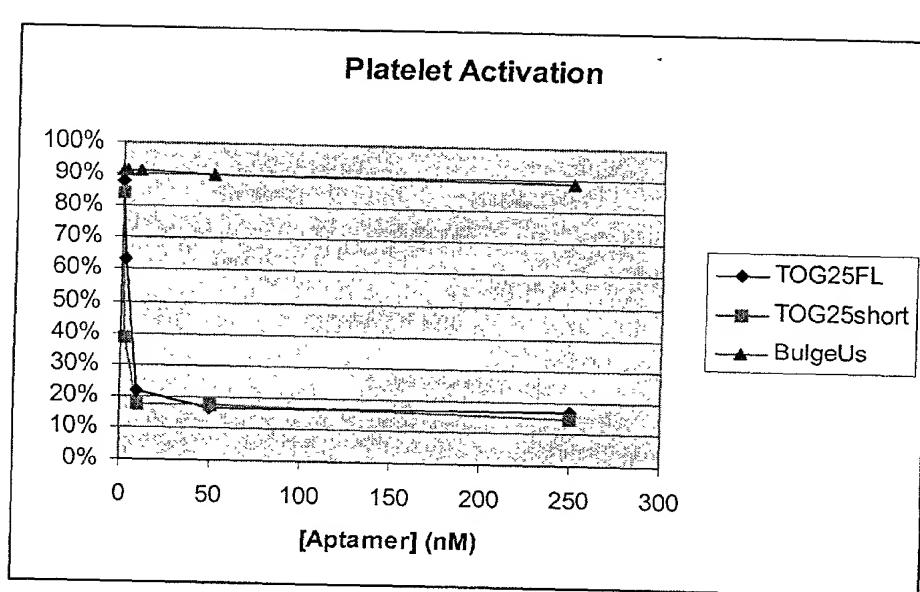


Figure 17  
E2F-3 Round 10 Aptamers

5' Primer GGG AGA GAG GAA GAG GGA UGG G (SEQ ID NO: 62)

3' Primer C AUA ACC CAG AGG UCG A A GUA CUG GA UCCC CCC (SEQ ID NO: 63)

10-1 and 10-8 (SEQ ID NO: 64)

5' P-AAU GGA AU C ACU GAA GCC CCU CCG UAG CAC CUA ACA CAG U-3' P

10-2 (SEQ ID NO: 65)

5' P-GCA UCC UGC CAG CGG CGA CGG ACC UUC GCC CAC AGG CC UU C-3' P

10-3, 10-7, 10-11, and 10-12 (SEQ ID NO: 66)

5' P-UUA UA AGC ACA CUG AAG CCC UCA GCA AAA CCU CCA CAG G-3' P

10-4 (SEQ ID NO: 67)

5' P-UAU GAA AU C ACA GAA GCC CGC GUU CGA CAC CUC CAC UGUU 3' P

10-5 (SEQ ID NO: 68)

5' P-CAA AC UAC AGA CUC CAA CUG CAG GAG CAC CCA CCC ACA CUG  
GGA CAG-3' P

10-6 (SEQ ID NO: 69)

5' P-AUC CCC GCC GUA AGC CGU CCU GAGGA CAC CAC ACU CCG C-3' P

	S1	L1	S2	L2	S2	L3	S1
*9-3 5'	gggauggggGA	CUAUACC	GCG	UAAUGC	UGC	C	UCCCCAUUCC
*9-20 5'	auggggGA	CUAUACCG	GCA	AUCG	UGC	A	UCCCCU
*9-25 5'	gggauggggGA	CCAUA	ACUC	UAAC	GGGU	GAA	UCCCGCAUCU
*9-26 5'	gggaugggg	UGAUA	ACCA	CUC	UGGU	GAA	CCCCUCCC
*9-28 5'	gggauggggCG	CCAUAC	GCA	CAU	UGC	UGCAU	CGCCUUCCC
*9-19 5'	gagggauggggA	CCAUA	ACGA	CUAC	UCGU	GAA	UCCCACCAUC
9-17 5'	gagggauggggA	CCAUAC	GCA	CAU	UGC	UGAA	UCCCCCUC
9-11 5'	gggauggggA	CUAUA	UUCGG	AAU	CUGGA		CUCCCACCU
9-4 5'	gggauggggCA	CUAUAC	GCA	UCU	UGC		UGCCUGCCC
9-16 5'	agggaugggg	CCAUA	CGU	GG	ACG	ACUGCA	CCCGACCCU
9-18 5'	gggaugggg	CCAUA	ACCA	CUU	UGGU	GAA	CCCACCCA
9-7 5'	ggaugggg	CGAUA	ACCA	ACA	UGGU	GAU	CCCAUUC
9-12 5'	gggaugggg	CGAUA	UAC	ACAUUG	GUG	AU	CCCACCC
9-2 5'	gggaugggg	CUAUUA	CAC	GCUG	GUG	AU	CCCAUCUC
9-14 5'	gggauggggGA	CUAUA	CGU	GAACG	ACU	GCA	UCCACUUCCC
9-27 5'	gggaugggg	UAAAUA	ACU	GUA	UGG	UGAA	CCCACCC

FIGURE 18

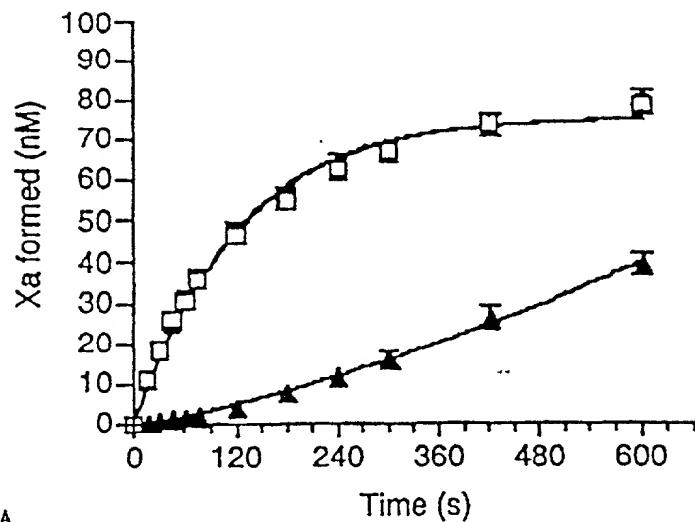


Fig. 19A

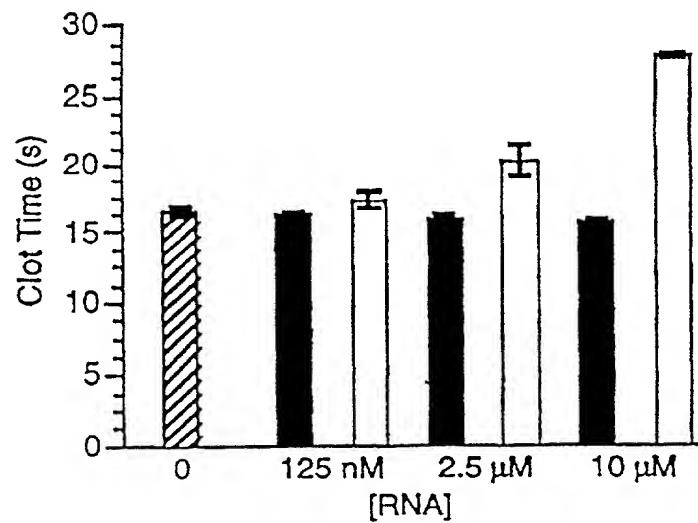
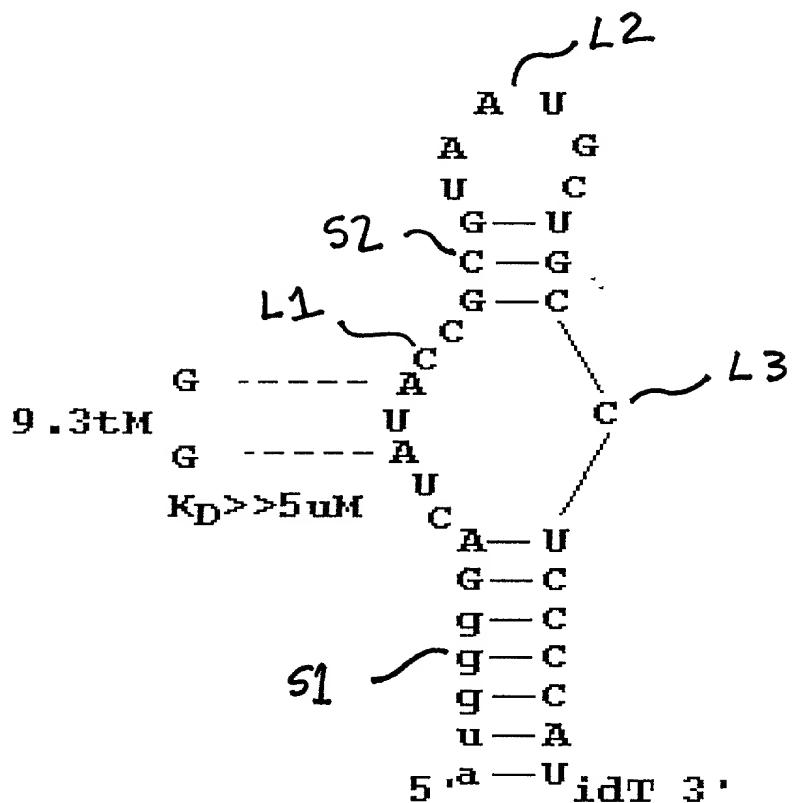
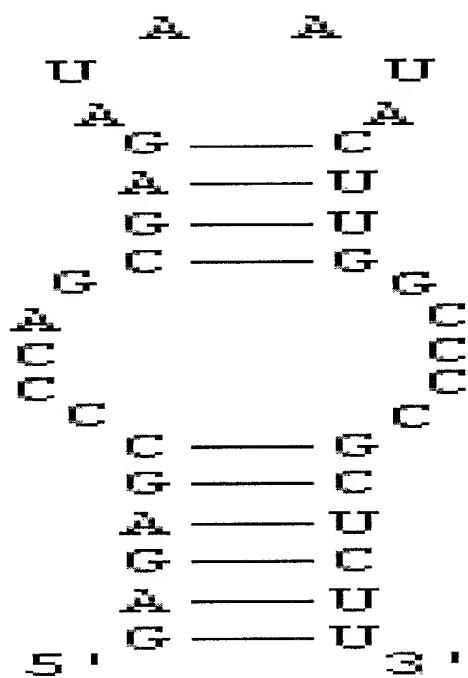


Fig. 19B

Figure 20



**Figure 21**



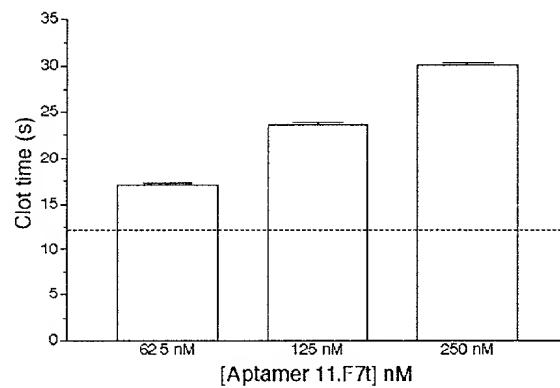


Figure 22A

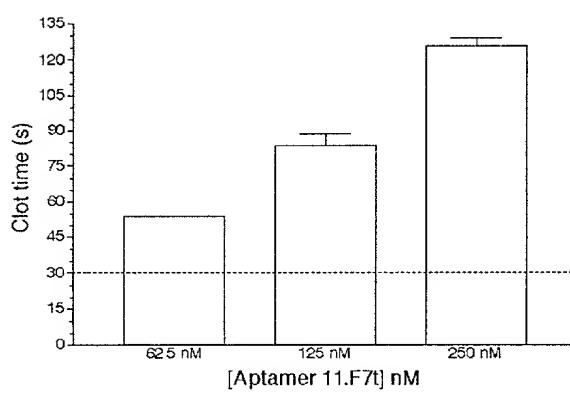


Figure 22B

Figure 23A

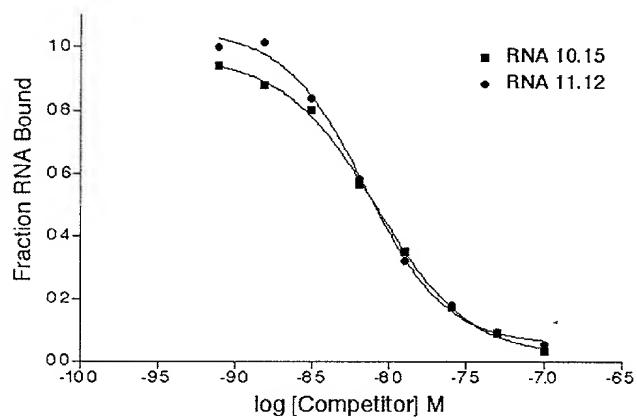


Figure 23B

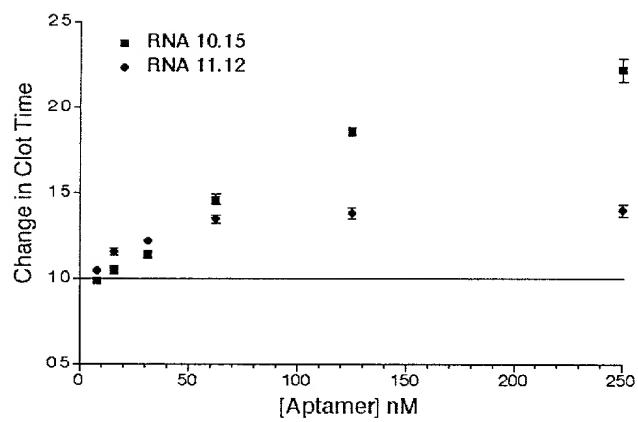


Figure 24

**ANG9-4 Binding**

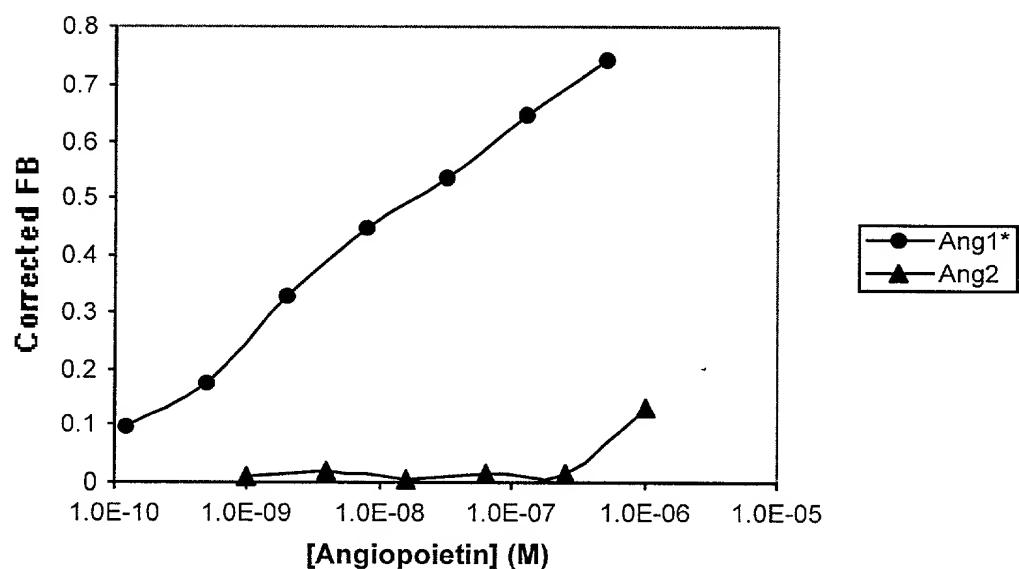
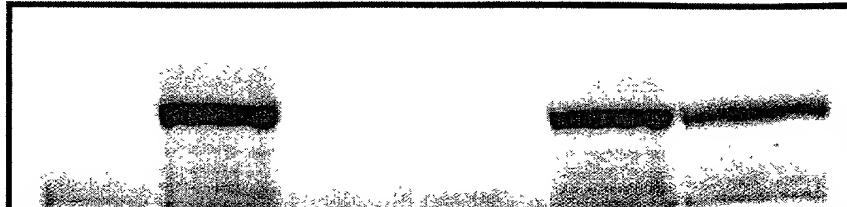


Figure 25

**blot:**

**pTie2**



**Tie2**



Ang1*:	-	+	+	+	+	+
fold-excess of aptamer:	0	0	10	100	10	100
aptamer:	none		9-4		control	

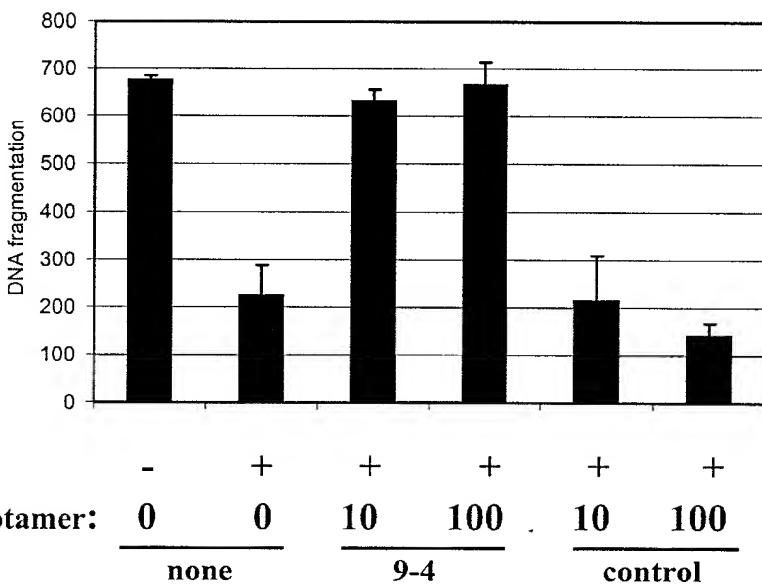


Figure 26

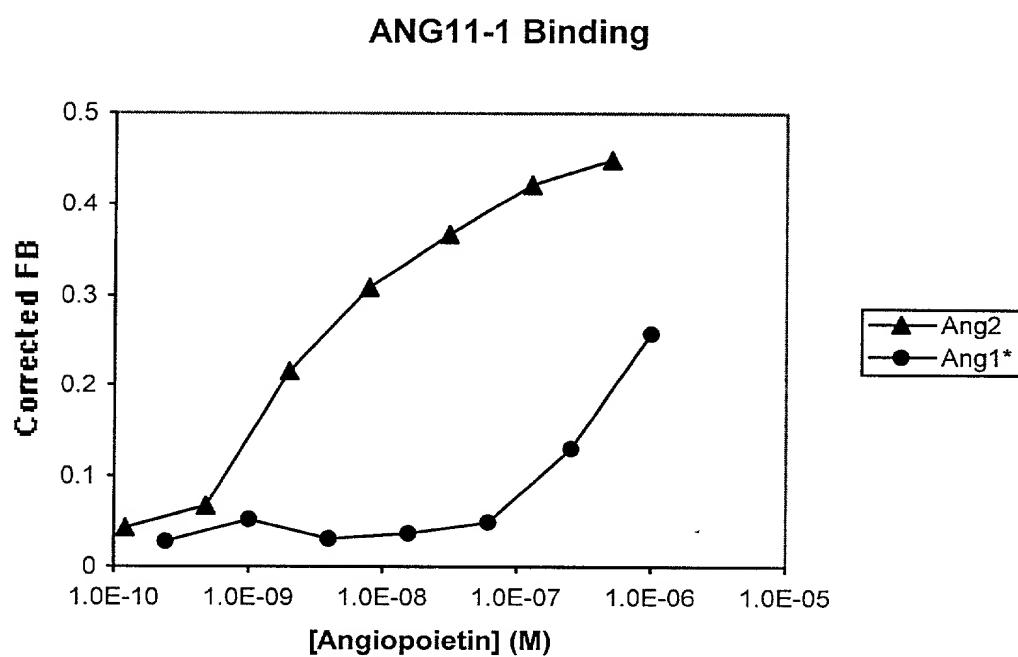


Figure 27

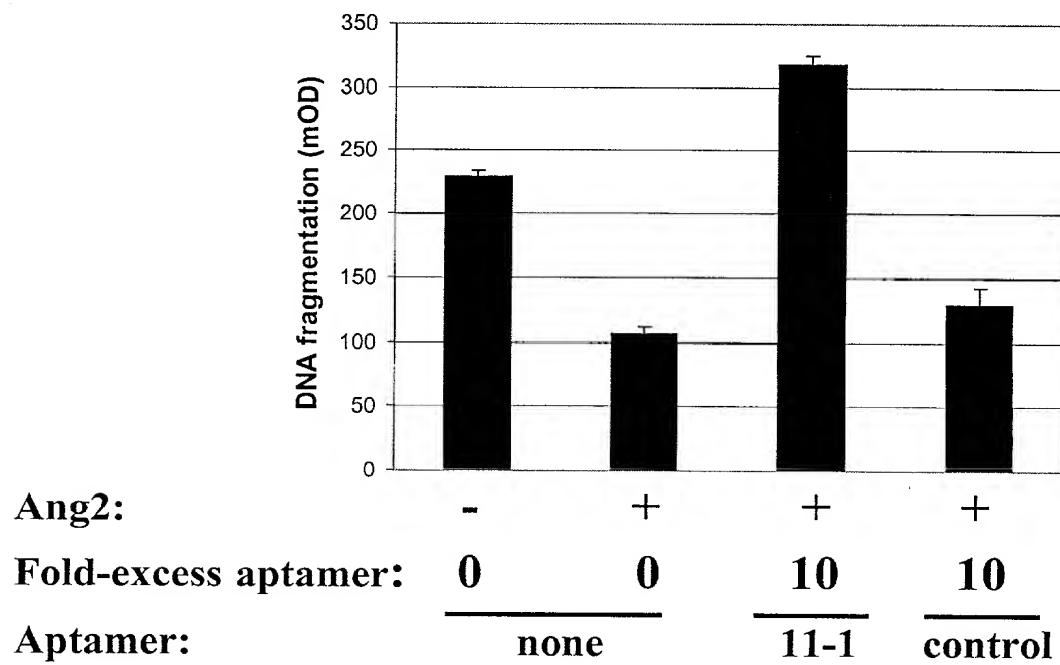


Figure 28

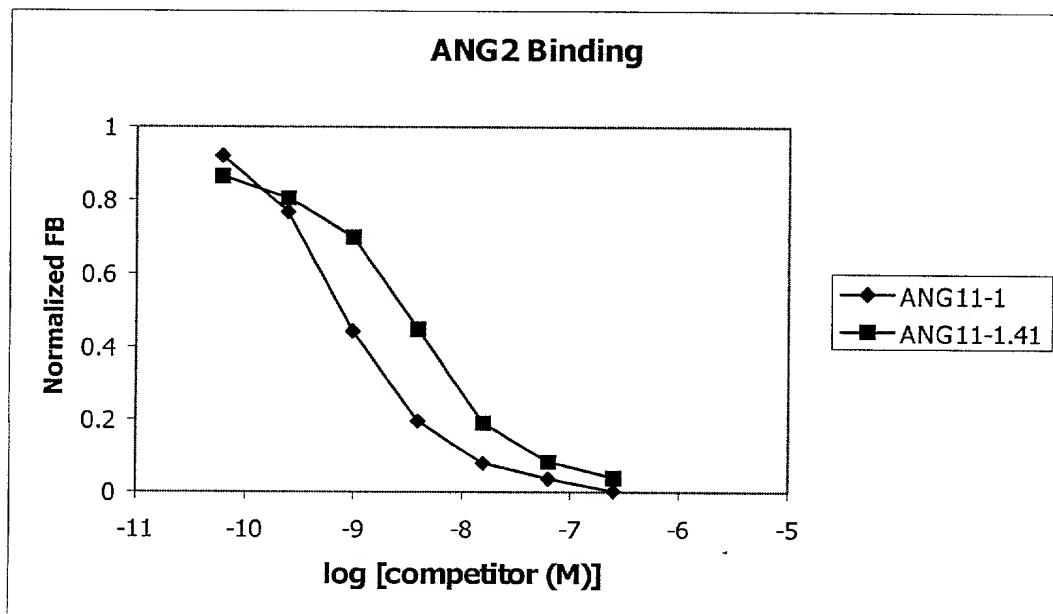
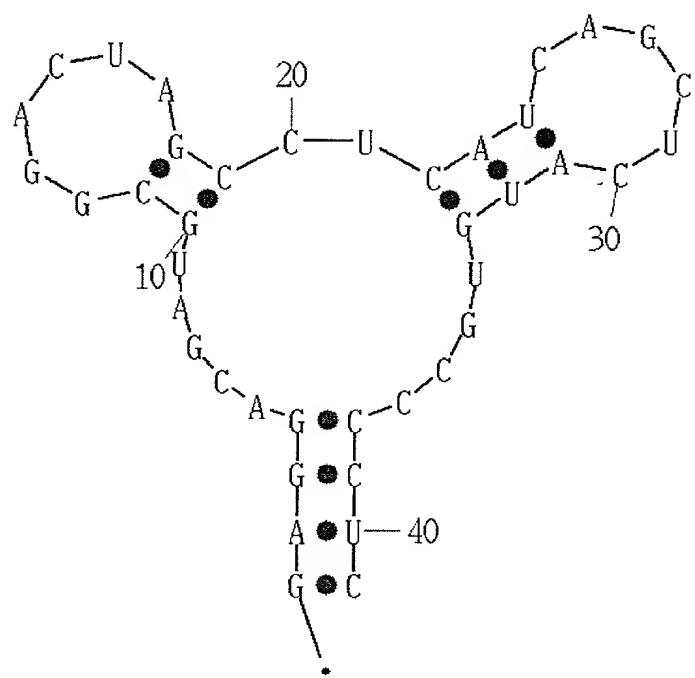


Figure 29

plt22.jpg by D. Stewart and M. Zuker  
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$$\Delta G = -1.43 \text{ [initially } -4.2] \text{ ANG11-1.41}$$

Figure 30

Figure 31

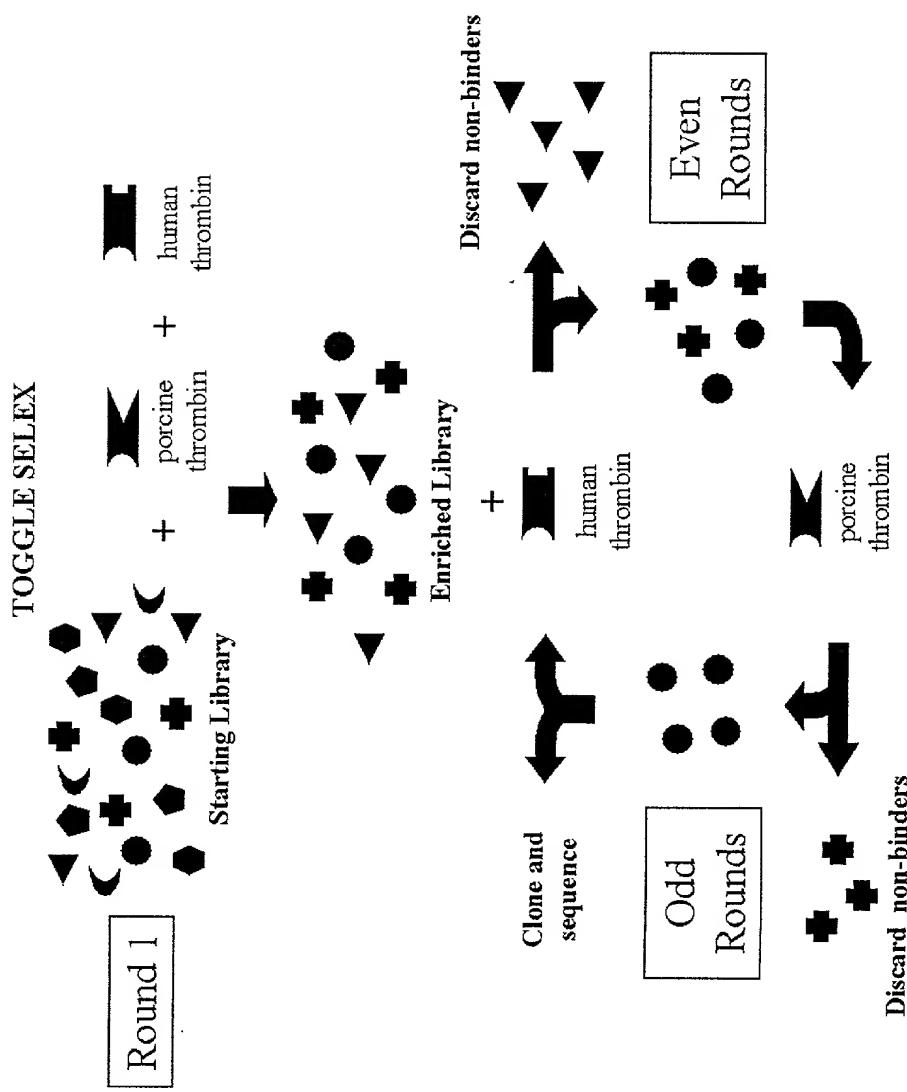


Figure 32

